

FIGURE 1

GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTGAGCCACACCAGGACTGT
GTTGAAGGGTGTCCCCCTAAATGTAATACCTCCTCATCTTCTTACACAGTG
TCTGAGAACATTACATTAGATAAGTAGTACATGGTGGATAACTCTACTTTAGGAGGA
CTACTCTCTGACAGCTCTAGACTGGTCTCTACACTAAGACACCATGAAGGAGTATGTG
CTCCTATTATTCCGGCTTGTGCTGCCAACCCCTTTAGCCCTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTTTCCAACAAAGAGAGCCAAGAAGCCATTTC
TTTGATCTGTTCCAATGTGTCATTGGATGTCAGTGCTATTCAAGGTTGTACATTGCTC
AGATTAGGTTGACCTCAGTCCAACCAACATTCCATTGATACTGAATGCTGATCTC
AAAACAATAAAATTAGGAAATCAAAGAAAATGATTTAAAGGACTCACTTCACTTATGGT
CTGATCCTGAACAACAAGCTAACGAAGATTCAACCCAAAAGCCTTCTAACCAAAAGAA
GTTGCGAAGGCTGTATCTGCCCACAATCAACTAAGTGAACATACCACTTAATCTCC
CATTAGCAGAACTCAGAATTGATGAAAATAAGTTAAGAAAATACAAAAGGACACATTCAA
GGAATGAATGCTTACACGTTGGAAATGAGTGCACCCCTCTGATAATAATGGGATAGA
GCCAGGGGCATTGAAGGGGTGACGGTGTCCATATCAGAATTGCGAGAAAGCAAAACTGAC
CAGTCCTAAAGGCTTACCAACTTATTGGAGCTTCACTTAGATTATAATAAAATTCA
ACAGTGGAACTTGAGGATTAAACGATACAAAGAACTACAAAGGCTGGGCTAGGAAACAA
CAAAATCACAGATATCGAAAATGGAGTCTGCTAACATACCAACGTGTGAGAGAAATACATT
TGGAAAACAATAAAACTAAAAAAATCCCTCAGGATTACCAAGAGTTGAAATACCTCC
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGAGTAAATGACTCTGTCCAACAGTGC
AAAGATGAAGAAATCTTATACAGTGCACAAAGTTATTCAACAAACCGGTGAAATACTGG
AAATGCAACCTGCAACATTGTTGTTGAGCAGAATGAGTGTTCAGCTGGAACTTT
GGAATGTAATAATTAGTAATTGGTAATGTCCTTAATATAAGATTCAAAATCCCTACATT
TGGAAACTTGAACTCTATTAAATAATGGTAGTATTATATAACAGCAAATATCTATTCT
AGTGGTAAGTCCACTGACTTATTGACAAGAAATTCAACGGAAATTGCAAACACTATT
GATACATAAGGGTTGAGAGAAACAAGCATCTATTGAGCTTCTTGTACAAATGAT
CTTACATAATCTCATGCTTGACCATTCCTTCTCATAACAAAAAGTAAGATATTGGTA
TTAACACTTGTATCAAGCACATTAAAAAGAACTGTACTGTAATGGAATGCTTGACT
TAGCAAAATTGCTCTTCATTGCTGTTAGAAAAACAGAATTACAAAGACAGTAATGT
GAAGAGTGCATTACACTATTCTTATTCTTAGTAACCTGGTAGTACTGTAATATTAA
CATCTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATCATGTCCTAGAGCC
CTTATGTTAAAATAATTCTAAAATAAGCCTCAGTAAATGTCATTACCAACTG
TAAATGCTACTCATAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTAATTATT
ACCTGATTTAAAATCTGTAAAAACGTGTAGTGTTCATAAAATGTAACCGCATT
AAATGATCCGTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATATAACATTGCC
TTCAACTCTAAGGAATATTGAGATATCCCTTGGAGACCTGCTTGGAGAGCCTG
CACTAACAAATTCTACACCAATTGTCTCTCAAATACGTATGGACTGGATAACTCTG
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCG
TATAAAATGCTCAGAGTTCTTATGTATTCTTATTGGCATCAACATATGTA
ACAGGGAAATTTCATTAAAATATTGGTTGAAAT

FIGURE 2

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392
<subunit 1 of 1, 379 aa, 1 stop
<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANI PRVREIHLENNKLKKIPSGLPEL
KYLQIIIFLHSNSIARGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM
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Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

FIGURE 3

CGGACGCGTGGCGGACCGTGGGCCGCGCACCGCCCCGGCCCTCCGCCCTCCGCACTCGCGCTCC
CTCCCTCCGCCGCTCCCAGCAGCTGCTCCGTCGCTGCCATGCCGAGCCTCC
GGCCCCGCCGGCCCCGCTGCTCCTCGGCTGCTGCCCTCCGGCCGGCCGCCAGA
GCCCGCGCTGCTGCCATCCGTTCTGAGAAGGAGCCGCTGCCCTGGAGCAGGCTGCACCTTCGGCG
GAAGGTCTATGCCTTGGACGAGACGTGGCACCCGACCTAGGGCAGCCATTGGGGTATGCGCTGCGTGTG
CGCCTGCGAGGCCTCAGTGGGTGCGCTACCAGGGCCCTGGCAGGGTCAGCTGCAAGAACATCAAACAGA
GTGCCAACCCGGGCTGTGGCAGCCGCCAGCTGCCAGACTGCTGCCAGACCTGCCAGGGAGCGCAG
CAGTCGGAGCGGCAGCCGAGCCGCTGCTTCAGTATCCGCGGGACCCGGAGCATCGCAGTTAGCAGCC
CGGGGAGCCAGGCCTGAGGAGCGGGCCCTGGTGACGGCACACGGACTTCGTGGCCTGCTGACAGGGCAG
GTCGCAGGCCTGGCACGAGCCCAGTCTCGCTGCGCTAGCCTCCGCTCTATCTCCTACAGGGCCT
GGACCGCCCTACCAGGATCCGCTCTAGACTCCAATGGCAGTGTCTGTTGAGCACCCCTGCAGCCCCCACCA
AGATGGCCTGGTCTGTGGGTGTCGGGGCAGTGCCTCGGTTGTCTCGGGCTCCTTAGGGCAGAACAGCTGCA
TGTGGCACTTGTGACACTCACTCACCCCTCAGGGGAGGTCTGGGGCCCTCATCCGGCACCGGGCCCTGGCTG
AGAGACCTCAGTGCCATCTGACTCTAGAACGGCCCCAACAGCAGGGCTAGGGGATCACCCCTGCTCACTCT
CAGTGCACACAGAGGACTCCITGCATTTTGCTGCTCTTCCAGGGCTGCTGGAAACCCAGGGAGTGGGGACTAAC
CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGCAGCTACTGCGAGAACTTCAGGCAATGTCTCAGCCCA
GGAACCAGGCTTGCTGAGGTGCTGCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGTGGGGAGCTGCA
GATGGCCCTGGAGTGGCAGGCCAGGGCTGCGCATCAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGT
CCTGCAAAGTGTCTTGCTGGGCTGATGCCCTGATCTACAGGTGCAAGTGGTAGGGACAAGCAGTGGAGGTGG
GAGACACTGGACAGGCTCAGGGAGGATCAGCGCACTGCTCTGCCCCATGGCTGGACTCCAGCCAGGAGGACAC
GGCGTGGGTATGCCCTGGCTGGGTGCCAGGGCTCATATGCTGCTGCAAGATGAGCTCTTCTGAACGT
GGGCACCAAGGACTTCCAGACGGAGAGCTCGGGGCACGGCTGCCCTGCCCTACTGTGGCATAGC
CCATGACACGCTGCCGTGCCCTAGCAGGAGCCCTGGTGTACCCCTGTGAAGAGCCAAGCAGCAGGGCACGC
CTGGCTTCTGGATAACCACTGTCACCTGCACTATGAAGTGCTGGCTGGCTGGCTGGCTAGAACAG
CACTGTCACTGCCAACCTCTGGCTGGGTGCCAGGGCTCGCGGCTGCTGAAGGGATTCTATGGCTC
AGAGGCCAGGGTGTGGTAAGGACCTGGAGCCGAAGTCTGGAGGGACTCCGAGGGCAGGTGACATAG
GATCACCACCAAGGGTAGCCCCAGAGGGAGCTCCGAGGGCAGGTGACATAGCCAACCAATGTGAGGTTGG
ACTGCGCTGGAGGGGCCGGGGCGAGGGGGTGGCGCTGGGGCTCCGGATACAGCCTCTGCTGCCGCC
TGTGGTGCCTGGCTCCGCCCTAGCGCCGCCAAACCTGGTGTCTGGGCCGGGGCGAGACCCAAACATG
CTTCTCGAGGGGCAGCGCCCCAACGGGCTCGCTGGGCCCAACTACGACCCGCTGCTCACTCTG
CTGCCAGAGACGAACGGTGATCTGACCCGGTGGTGTGCCACCGGCCAGCTGCCACACCCGGTGCAGGCTCC
CGACCAAGTGTGCCCTGTTGCCCTGAGAACAAAGATGTCAAGAGACTGCCAGGGCTGCCAGGGAGGCC
AGGAGAGGGCTGCTATTGTGACGGAGCTGGGGCAGCGGGTACGGTGGCAGCCGGCTTGTGCCCC
CTTGGCTTAATTAGTGTGCTGCAACCTGCAAGGGGGCACTGGAGAGGTGACTGTGAGAACGGTGCAGTG
TCCCCGGCTGCCCTGTGCCACGGCTGTGCGTGTCAACCCACCGACTGTCGAAACAGTGTCCAGTGGGTG
GGCCACCCAGCTGGGGACCCCATGCAAGGCTGATGGGCCGGGGCTGCCGTTTGCTGGCAGTGGTCCC
AGAGAGTCAGAGCTGGCACCCCTAGTGCCTTGGAGAGATGAGCTGTATCACCTGCAAGATGTGGGG
GGTGCCTCACTGTGAGGGGATGACTGTTCACTGCCACTGTCCTGTGGCTGGGGAGAGAGTCAGTGTG
CCGCTGCAGGCCACGGCGCCCCAGAGACCAACTGATCCAGAGCTGGAGAACAGCCGAAGGCTCTA
GGGAGCAGCCAGAGGGCAAGTGAACCAAGAGGATGGGGCTGAGCTGGGGAGGGTGGCATCGAGGACCTT
GCATTCTCTGTGGGAAGCCCAGTGCCTTGTCTCTGTCTGCCACTCCACCCACCCACTACCTCTGGAA
CCACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCTGCC
TCGGCCTCTGTGCTGGAGGCCACCCCTTCTGTACATAATGTCAGTGGCTGGGATTAAATT
TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG
TTTGTATTATAAACATTCTTTCAAGTCAAAAAAAAAAAAAAAA

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLGLLLLGSRPARGAGPEPPVLPIRSEKEPLPVRAAGCTFGGKVYALDE
TWHPDLGQPFGVMRCVLCACEAPQWGRRTRGPGRVSKNIKPECPTPACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAERARGDHTDFVALLTGPRSQAVAR
ARVSLLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEPAAPTQDGLVCGVWRRAVPRLSLRL
LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTLSDTED
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPEGFAEVLPNLTQEMD
WLVLGELQMALEWAGRPGRLISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML
LQNELFLNVGTTKDFPDGELRGHVAALPYCGHSARHDTPVPLAGALVLPPVKSQAAGHAWLS
LDTHCHLHYEVLLAGLGGSEQGTVAHLLGPPGTPGPRRLKGFYGSEAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGLRLEAAGAEGRALGAPDTASAAPPVV
PGLPALAPAKPGGPGPRDPNTCFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCP
PPSCPQVQAPDQCCPVCPEKQDVRDLPGLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPF
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVRVNPTDCKQCPVGSAGHPQLGDPMQADG
PRGCRFAGQWFPEQSWHPSVPPFGEMSCITCRCAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGCGCCGTCACTGCG
TCCGGCTCCGGCTCCCGGCCCTCCGGCCGGCCATGCAGCCCCGCCGCCAGGCGCCCGGTGCGCAGCTGC
TGCCCGCCGCTGGCCCTGCTGCTGCTGCTGCCAGGGGCCGGAGGCAGCTCCCTGCCAACCCGGTGCCCCG
CCGCGCCCTTGTCTGCGCCGGCGCAGCCCTGCCGAATGGGGGTGTGCACTCGCACCTGCCGGATCTCCGGCG
AGCCGGACCCCGCAGCACCCGGCCCCGCCGGCAGCCTGGCTACAGCTGCACCTGCCCGCCGGATCTCCGGCG
CCAAC TGCCAGCTTGTGCA GAT CCTTGTGCCAGCA ACCCTTGTCA CCATGCCA ACT GCAG CAG CAG CAG
GCAGCAGCGATGGCTACCTCTGCATTGCAATGAAGGCTATGAAGGTCCA ACT GTGA ACAGGCA CT TCCCAGTC
TCCCAGCCACTGGCTGGACCGAATCCCATGGCACCCGACAGCTCAGCCTGTTCTGCTACTCAGGAGCCTGACA
AAATCCTGCCTCGCTCTCAGGCAACGGTACACTGCCCTACCTGGCAGCCAAAACAGGGCAGAAAGTTGAGAAA
TGAAATGGGATCAAGTGGAGGTGATCCCAGATATTGCCCTGTTGGGAATGCCAGTTCTAACAGCTCTGCCGGTGGCC
GCCGGTATCCTTGAAGTGCACAGAACACCTCAGTCAGTCAGATTGGCAAGATGCCACTGCCCACTGATTG
TCTGGAAGGTACGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT
CAGGGGGACTGGCTCTGGAGGAGATGCTGCCCTGGGAATAATCACTTTATTGGTTTGATGATTCTG
TGACTAAGTCTATTGGCTTGCGCTTAACCTCTGGTGGTGAAGGTACGCACCTGTGTCGCCGGGAGAGTCACG
CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGACCAACAGCGTCAGAGGCAACTTTTCCAGTCTCAGTGGAT
AGGAGCAGTACGTGGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTTGCACAAACAGCGAGCT
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTCACCTGTGTTGCCCTGGTTACTGGAGAGCTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGAGAAAAGGTGGACCCCTGCCCTCGTCTCCGT
GCCAGAACACGGCACCTGCTATGTGGACGGGTACACTTACCTGCAACTGCAGCCGGCTTCACAGGGCGA
CCTGTGCCAGTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCGAGCGTGGCACAGC
ACAAATGCCCTGTGATCCAGTTACATGCCCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
GCCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTCCTGGCAGAACATCAAAGGAACAC
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CCTGCCACCATGGGGAGCTGCCCTGGACCAGCCCAATGGTTATAACTGCCACTGCCGCATGGTTGGGGAG
CAAAC TGAGATCCACCTCAAATGGAAGTCCGGCACATGGCGAGAGCCTCACCAACATGCCACGGCACTCCC
TCTACATCATCATTGGAGCCCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGATTGCCGA
TCAGCCGCATTGAATACCAGGGTTCTTCAGGCCAGCCTATGAGGAGTTCTACAAACTGCCGAGCATCGACAGCG
AGTTCAAGCAATGCCATTGCAATCCGCATGCCAGGTTGGAAAGAAATCCGGCTGCAATGTATGATGTGA
GCCCATGCCCTATGAAGATTACAGTCTGATGACAACCCCTGGTCACACTGATTAACAAAGATTGTAAT
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GAAATTAAATGCTAGCTCAAGAGTTTCAGTAGAATATTAAAGAACTAATTCTGCACTTTAGTTG
GAAAAAATATTTAAAACAAAATTGTGAAACCTATAGACCGATTTTAATGTACCTTCAGCTCTCAAATGT
GTGCTTCTACTAGTGTGCTCTTCACTGTAGACACTATCACGAGACCCAGATTAAATTCTGTGGTTGTTACA
GAATAAGTCTAATCAAGGAGAAGTTCTGTTGACGTTGAGTGCCTCTGAGTAGAGTTAGGAAAACCAC
GTAACGTAGCATATGATGTATAATAGAGTATACCGTTACTTAAAAGAAGTCTGAAATGTCGTTTGAA
AGAAAATAGTTAAATTACTATTCTAACCGAATGAAATTAGCCTTGCCTTATTCTGTGCACTGGTAAGTAAC
TTATTCTGCACTGTTGTTGAACCTTGTGAAACATTCTTCAGGTTGTTGTCATTTCGTAACAGTC
TCGAACTAGGCCTAAAAACATACGTAACGAAAAGGCCAGCGAGGCAAATTCTGATTGATTGAACTATATT
TTCTTAAAGTCAAGGGTTCTATATTGTGAGTAATTAAATTACATTGAGTTGTTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTCCCTCAGTAGTGAGTATTCTCATAGTGCACTTATTATCTCCAGGATGTT
TTTGTGGCTGTATTGATTGATATGTGCTTCTGATTCTGCTAATTCCAACCATTGAAATAATGTGATC
AAGTC

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQQLPALLLLLLGGAGRGSSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDHQHPAPAGEPGYCTCPAGISGANCQLVADPCASNPCHGNCSSSSSSDGYLCICN
EGYEGPNCEQALPSLPATGWTEMAPRQLQPVPATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGLVLLEEMLALGNNHFIGVNDSVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTPSEATFSCTCEEQYVGTFCCEYDACQRKPCQNNASCIIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC
ASSPCQNNGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSGVTSYKCLCDPG
YHGLYCEEYNECLSAPCLNAATCRDLVNGYECVCLAELYKGTHCELYKDPCANVSLNGATC
DSDGLNGTCICAPGFTGEEDIDINECDSNPCHGGSCLDQPNGYNCHCPHWVGANCEIHL
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKKSRPAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTACGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGCTTCAGGGGACTGGCCTCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGTACTTCTGTGAAGAACGATGCTGCCAGAGGAAACCTGCCAAACAAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTCACCTGTGTTGCCCTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

FIGURE 8

CTCTGGAAGGTACGGCACAGGATTCCAACAGTGCCTCCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGTTCAAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAAGAGGCAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGTACTTCTGTGAAGAACAGATGCTGCCAGAGGAAACCTGCCAAACAAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTACCTGTGTTGCCTTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

FIGURE 9

GCTGAGTCTGCTCCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCAACGCTGGCGCCCCAGAGCCCACACCATGCCGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGCCCT
GATGCGGACTTCCGCTCGTGGACGCCACAACGACCTGCCCTGGTCCTAAGGCAGGTTT
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AGGCTTAGAGATGGCCTCGTGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCCCTGGAGCAGATTGACCTCATGCCCATGTGCGCT
CCTATTCTGAGCTGGAGCTTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
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GCTCCGCTAAGGGGTCCACTCCTCTACAACAAACATCAGGGCTGACTGACTTTGGTAG
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GGGGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTCTGAAGAAGAAC
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GTCCACTGTGGCAGATCACTCGACCACATCAAGGCTGTATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGCCGCAAATTCCCTCAGGGCTGGAAGACGTGTCACATAC
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCC
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TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACACTGAGATTCCCATA
CTGGACAGCCAAGTTACCAAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG
TCCTTGCAGTTGTGGCACCTTCCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA
AATATTCCCTGAAATAATGTTGGACATAG

FIGURE 10

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pI: 6.11, NX(S/T): 5
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QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTHTCNPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLRQLRQSLTSGQELTEIPIHWTAKLPAKWSVSESSHMAPVLAFFPVLIWL
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N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACCTATAATATTCCGGATTATTACCGTCCCACCATGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCTGATGCGGGACTCCGCTGTGGACGGCAC
AACGACCTGCCCTGGTCCTAAGGCAGGTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTCAGCTACGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGCGCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTACCCCTGGAG
CAGATTGACCTCATGCCGCATGTGTGCCCTATTCTGAGCTGGAGCTTGACCTCGC
TAAAGCTCTGAACGACACTCAGAAATTGCCCTGCCTCATCGGTGTAGAGGGTGGCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGAGTGCCTACCTGACGCTC
ACCCACACCTGCAACACACCCCTGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCACTCGGCTGCCGGGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTCGACCACATC
AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGCCGGCAAATT
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GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTGGAGGACAAGTTCCCGATGA
GCAGCTGAGCAGTCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAAGCCAAGTGGTCA
GTCTCAGAGTCCTCCCCCACCCTGACAAAACTCACACATGCCACCCTGCCAGCACCTGA
ACTCCTGGGGGACCGTCAGTCTTCCCTCTCCCCCAAAACCCAAGGACACC

FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T) : 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSDLNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDKTHTCPCCPAPELLGGP
SVFLFPPPKPKDT
```

FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCGGCCCTCCCGCGCCCGGCCCTGCGTCCCGGCC
CTGCGCCACCGCCGCCGAGCCGAGCCCCGCCGCGGCCCTGGCAGCGCCGCCATGCC
GCCGGCCGCCGGGGCCCCGCCAATCCGCGGGCGGCCGTTGCTGCCCTGCT
GCTGCTGCTCTGCGTCCTCGGGCGCCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCACCTGCTCAGTGCACGGA
GACCCACCAGGAGCCACCGCCGAGGGCTACTGGACCCCTAACGGCGCCCTGCC
TGAGCTCTCCCGTGTACTCAACGCCCTCACCTGGCTCTGCCCTGGCCAACCTCAATGGGT
CCAGGCAGCGGTGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATTGGCTGGC
TCCTGCCCTATGTTGGCCTGCCAGAGAAACCGTCAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGAGACCTCCTCACACCCA
ACTACTCCCTCAAGTACAAGCTAGGTGGTATGCCAGGACAACACATGTGAGGAGTACAC
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTTACGCCCTATGAGAT
CTGGGTGGAGGCCACCAACGCCCTGGCTCTGCCGCTCCGATGTACTCACGCTGGATATCC
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGCACGTGAGCCGCGTGGGGCCTGGAG
GACCAGCTGAGCGTGCCTGGTGTGCCACCCGCCCTCAAGGATTCCCTTTCAAGCAA
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA
ACCAGACCTCCTGCCCTGGCCGCTGAAACCCGGCACCGTGTACTCGTCAAGTGC
TGCAACCCCTTGGCATCTATGGCTCCAAGAAAGCCGGATCTGGAGTGAGTGGAGCCACCC
CACAGCCGCTCCACTCCCCGAGCTGGGGCCGGTGCAGCGAGCTCAAGCAGTCCCTGGCTGGCTC
GGGGCGAGAGCCGAGCTGGGGCCGGTGCAGCGAGCTCAAGCAGTCCCTGGCTGGCTC
AAGAACGACCGTACTGCTCCAACCTCAGCTCCGCTCTACGACCAAGTGGCGAGCCTGGAT
GCAGAACGTCGACAAGACCCGCAACCAGGACGAGGGATCCTGCCCTGGCAGACGGGCA
CGGCAGAGAGGTCCCTGCCCAGATAAGCTGTAGGGCTCAGGCCACCCCTGCCACGTGGAGA
CGCAGAGGCCAACCAAACGGGCCACCTCTGTACCCCTACTCAGGGCACCTGAGCCAC
CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCCAACGCCATAACAGCTCTGACTCCACGT
GAGGCCACCTTGGTGCACCCAGTGGTGTGTGTGAGGGTTGGTTGAGTTGC
CTAGAACCCCTGCCAGGGCTGGGGTGAGAACGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCCTTAAATAAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAACAAAAAAA

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRGPAAQSARRPPPLPLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCKNMKDLTCRWTGAHGETFLHTNYSLKLRWYGQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRRLGSARSDVLTLIDLDVVTTDPPPDVHVSRVGG
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVWKVVDDVSNQTSCRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSGPVRRELKQFLG
WLKKHAYCSNLFSRLYDQWRAMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

FIGURE 15

FIGURE 16

```
</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436
<subunit 1 of 1, 300 aa, 1 stop
<MW: 32964, pI: 9.52, NX(S/T): 1
MKFLLDILLLPPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ
```

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 17

GAATGAGCTGGAGTCTGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAAGGACTG
GGGTGACGGCAGGGCAGGGCGCCTGGCCGGGAGAAGCGCAGGGCTGGAGCACCAACAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATGGGAGCCGGAGGGGGACT
GCGAGAGGACCCGGCGTCCGGCTCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCTGC
TGCTCCTGGCCTGGCGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGCACCCGGCCTTCAGGCACGCCGGCCACCATGGCAGCCAGGGCTGCCGGGCCG
CGATGGCCGCGACGGCCGCGACGGCGCGCCGGGCTCCGGAGAGAAAGGCAGGGCGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCGGGCCGAGGAGAGGCAGGGACCCGGGG
CCCACCGGGCCTGCCGGGAGTGCTCGGTGCCTCCGCATCCGCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCCTGCCCTCGACCGCGTGCTGGTGAACG
AGCAGGGACATTACGACGCCGTACCGGCAAGTTCACCTGCCAGGTGCCTGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCAGCCTGCAGTTGATCTGGTGAAGAATGGCGA
ATCCATTGCCCTTTCTTCAGTTTCGGGGGTGGCCAAGCCAGCCTCGCTCTCGGGGG
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGTGAGGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTCTCCGGATTCTGGTGTACTCCGA
CTGGCACAGCTCCCCAGTCTTGCTAGTGCCACTGCAAAGTGAGCTATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTATCCAGGAGGGCTGGCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGTAGAGCACTCTCCGTCTGCTGGCAAGGAATGGGAAC
AGTGGCTGTGCGATCAGGTCTGGCAGCATGGGCAGTGGCTGGATTCTGCCAACGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGCCAGGAGCCCACGGT
GGGGTGCCTCTGGCCTCTGCTCTGGATCCTCCCCACCCCTCCTGCTCCTGG
GCCGGCCCTTTCTCAGAGATCACTCAATAAACCTAAGAACCCCTCATAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 18

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592
><subunit 1 of 1, 243 aa, 1 stop
><MW: 25298, pI: 6.44, NX(S/T): 0
MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHGSQGLPGRDGRDGRDGAPGAP
GEKGEGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRV LVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQWVQVGVDYIGIYASIKT DSTFSGFLVYSDWHSSPVFA
```

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTCTGCTCCTCCCTGCACAACCGCCTGCGCAGCTGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCACCAGGGCAGCCCTGTGGAATCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCTG
CAAGTGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCCTTGTGAAGTGGTCAG
CCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGCCACCTCAAGCCAGCTGGCTGTGGCGGAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAACGCCTTGTCTGTGCCTACTCCCCGGAGGCAA
CTGGGAGGTCAACGGAAAGACAATCATCCCATAAGAAGGGTGCCTGGTGTGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGACATGCAGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACATGGACGTCTAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTG
ACGGCCGGTTCCGGAGGAGGAGTGTGCTCGTGTGACATCGGCTACGGGAGGCCAG
TGTGCCACCAAGGTGCATTTCCCTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAGGCG
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTGCCCTATCTGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATCGGCT
CACCTACAAGACGCCAAGGACTCCTCCGCTGGCCACAGGGAGCACCAGGCCTCACCA
GTTTGCCCTTGGCAGCCTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCCTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCAGGGCCT
GAGGCCTGACCACATGGCTCCCTGCCCTGGAGCACCAGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCAGGTTAAGACCACATGCCATGTCAAAGAGGTCTCAGA
CCTTGCACAATGCCAGAAGTTGGCAGAGAGAGGAGGGAGGCCAGTGAGGGCAGGGAGTG
AGTGTAGAAGAAGCTGGGCCCTCGCCTGCTTTGATTGGAAAGATGGCCTCAATTAGA
TGGCGAAGGAGAGGACACCGCAGTGGTCAAAAAGGCTGCTCTTCCACCTGGCCAGAC
CCTGTGGGCAGCGGAGCTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

FIGURE 20

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176
<subunit 1 of 1, 455 aa, 1 stop
<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQQAPMAGALNRKESFLLSLHNRLRSWV
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLNISTCH
CHCPPGYTGRYCQVRCSSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYYRARMKCQRKGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGPGS

Signal sequence.
amino acids 1-26

Transmembrane domain.
amino acids 110-124

N-glycosylation sites.
amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 45-49

N-myristoylation sites.
amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 204-215

EGF-like domain cysteine pattern signature.
amino acids 249-261, 280-292

C-type lectin domain signature.
amino acids 417-442
```

FIGURE 21

CGGACGCGTGGGCTGGCGCTGCAAAGCGTGTCCGCCGGTCCCCGAGCGTCCCGCGCCCT
CGCCCCGCC**ATG**CCTGCTGCTGGGCTGTGCCTGGGCTGTCCCTGTGTGGGTCGCA
GGAAGAGGCCAGAGCTGGGCCACTCTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG
TCAGACTGTTGAGAGGCTGAAAACCAACCTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTCCCGTTATGCCTCACTACGGTTCTGAGAATGCTAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTCATCACCAACTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGTAGG
GTAAAAGAGAAAAGGAATAAAACACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTAG
AGCTTCTGCAGTGATTCCCAGCAAGGACAAAGCCGCTTTCTGAGTTATGAGGAGCTTC
TGCAGAGGCCCTGGCAAGTACGAGCACAGCATCAGCGTGCAGGCCAGCAGCTGTCCGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCAGAGGGCAGTGGCGGGGAAGATGATTCTGGCCTCCCCAT
CTACTGTCATTAACCAAAATGAAACATTGCCAACATAATTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCAGAATGGAATTGGAGACTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGACATCCAGGTTCAAATGGCTATTGTGCACTACTTGCTCCTA
AAGACCTTCCTCCTTACCCAAGAATGTGGTATTGTGCTTGACAGCAGTGCTTATGGT
GGAACCAAACCTCGGCAGACCAAGGATGCCCTTCACAATTCTCCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTGGATTTCACCGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGAAAGTGTACATTACCATATGTCACCCACTGGA
GGCACAGACATCAACGGGCCCTGCAGAGGGCATTAGGCTCCTAACAAAGTACGTGGCCA
CAGTGGCATTGGAGACGGAGCGTGTCCCTCATCGTCTTGACGGATGGGAAGCCACGG
TCGGGAGACGCACACCCCTCAAGATCCTCAACAAACACCGAGAGGCCGCCCCAGGCCAGTC
TGCATCTTCACCATTGGCATCGCAACGACGTGGACTTCAGGCTGCTGGAGAAAATGTCGCT
GGAGAACTGTGGCCTCACACGGCGTGCACGAGGAGGACGCAGGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCCGCTCTCTGACATCCGATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCCCTGTCACACTACTCAACGGCTGGAGATCATCAT
TGCGGGAAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTACCGCCAGCAACA
GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCAGGCCCTCAGAAGGAGGGAAAGAT
GTCACAGGAAGCCCGAGGCCTGGAGGCGATGGAGAGGGGACACCAACCACATGAGCGTCT
CTGGAGCTACCTCACCAAAAGGAGCTGCTGAGCTCTGGCTGCAAAGTGAAGATGACGG
AGAAGGAGCGCTGCCAGGGGCCAGGCCCTGGCTGTGAGCTACCGCTCCTCACTCCC
TTCACCTCCATGAAGCTGAGGGGCCGGTCCCACCGCATGGATGGCCTGGAGAGGCCACGG
CATGTCGGCTGCCATGGACCCGAACCGGTGGTGCAGAGCGTGCAGGAGCTGGCACGCAGC
CAGGACCTTGCTCAAGAAGCAAACCTCCGTCACAAAAAAACAAAACAAAACAAAAAAGA
CATGGGAGAGATGGTGTGTTCTCCACCACTGGGATACGAT**G**AGAAGATGGCACCT
GCAAGCCAGGAAGACGCCCTCACAGACACCATGTCGTGGCACCTTGATCTGGACCTC
CCAGCCTCCAGAACTGTGAGAAATAATGTGTTAAGCTAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192
<subunit 1 of 1, 694 aa, 1 stop
<MW: 77400, pI: 9.54, NX(S/T): 6
MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLKTKPLMTEFSVKSTIIS
RYAFTTVSCRMLNRASEDQDIEFQMGI PAAAIFTNFTMLIGDKVYQGEITEREKSGDRVKE
KRNKTTTEENGEGTEIFRASAVIPS KDKAAFFLSYEELLQRRLGKYEHSISVRPQQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANII FKPTVVQQAR
IAQNGILGDFI IRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGTK
LRQTKDALFTI LHDLRPQDRFSI IGF SNRI KVWKDH LISVTPDSI RDGKVYI HHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNNTREAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEIIIAGKLVDRKLDHLHVEVTASNSKKFI ILKTDVPVRPQKAGKDVTG
SPRPGGDGE GTDNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKQNKT KKRHGR
DGVFPLHHLGIR
```

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGGGTGCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGCGGCCGGCGCCTCCCGGGCTCCGGCTCTGCTGTTGCTCTCTCCGCCGCG
CACTGATCCCCACAGGTGATGGCAGAATCTGTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCACAGGTGATGGCAGAATCTGTTACGAAAGACGTGACAGTGATCGAGGGA
TCCCAACAGGCAGACCATTATTCAGGGACTTCAGGCCTTGAAGGCAGCAGGTTTCAGT
TGCTGAATTTCAGTGAACCAAAGTATCATTGACAAACGTCTCAATTCTGATGAA
GGAAGATACTTTGCCAGCTCTACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTCAAA
GGGAACACAGAGCTAAAGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGACAAGGAGGACGATGGGTCCCAGTGATCTGCCAGGTGG
AGCACCCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGACATTCACTGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCCCTGA
GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGTAACGGTGGTGGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCAACCTGTTCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTCAAACATAGTGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACATCCCTCCTCCCACAACAACCACCA
CCACCACCACCACCACCATCCTTACCATCATCACAGATTCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGGCCAT
GCTGTGCTTGCTCATCATTCTGGGCGCTATTTGCCAGACATAAAGGTACATACTCACTC
ATGAAGCCAAGGAGCCGATGACCGCAGCAGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCATCTAGATCAGCTTTGTGTTCAAT
GAGGTGTCCAACTGGCCCTATTTAGATGATAAAGAGAGACAGTGATATTGG

FIGURE 24

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
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MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEIEVNCTAMASKPATTIRWFKGNTTELKG
KSEVEEWSDMYTVTSQMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTNGTYR
CEASNIVGKAHSDYMLYYDPPTTIPPPTTTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGYFTHEAKGADDAADADTAIIINAEGGQNNSEE
KKEYFI
```

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCGA
CCCGCCAGGAAAGACTGAGGCCGCGCCTGCCCGCCGGCTCCCTGCGCCGCCGCCCTC
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGCCCT
GGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAAGCCAGCACAGACAGTCTTCT
GCACTGCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGCTGTAC
GTCTTGAGAACGGCATCACCATGCTCGACCGAACGAGCTTGCAGGCCCTGCCGGGCTGCA
GCTCCTGGACCTGTACAGAACCGAGATGCCAGCCTGCCCTGCCCCGCTGCTGCTGG
ACCTCAGCCACAACAGCCTCTGGCCCTGGAGCCGGCATCCTGGACACTGCCAACGTGGAG
GCGCTGCCGCTGGCTGGCTGGGCTGCAGCAGCTGGACGAGGGCTCTCAGCCGCTGCG
CAACCTCCACGACCTGGATGTGCTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCTCCGGGGCCTGACGCCCTGCCCTGGAGCTGGACGAGGGCTCTCAGCCGCTGCG
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGAACCTAACGCTGCC
CCTGCCTGGCACCTCTGGCCTCTTCCCCGCCCTGCCCTGCGCTGCTGGCAGCTGCCGCAACC
CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTGGCCCTGGTGCAGGAGAGGCCACGTGACA
CTGGCCAGCCCTGAGGAGACGCCCTGCCACTTCCCAGCAAGAACGCTGGCCGGCTGCTCCT
GGAGCTTGACTACGCCGACTTGGCTGCCAGCCACCACACCACAGCCACAGTGGCCACCA
CGAGGCCCGTGGTGCAGGAGCCACAGCCTTGCTTCTAGCTTGCTCCTACCTGGCTTAGC
CCCACAGGCCGCCACTGAGGCCAGGCCCTACACCAGTCAGCCGAGGCCACCACGGCC
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCCTCAATGGGGCACATGCCACCTGG
GGACACGGCACCACTGGCTGCTTGCCCCGAAGGCTCACGGCCTGTACTGTGAGAGC
CAGATGGGGCAGGGACACGCCAGGCCCTACACCAGTCAGCCGAGGCCACCACGGCC
GACCCCTGGCATCGAGCCGGTGAACGCCACCTCCCTGCCGTGGGCTGCAGCGCTACCTCC
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATGGGCC
AAGCGGCTGGTACGCTGCCACTGCCCTCGCTGAGTACACGGTACCCAGCTGCC
GCCCAACGCCACTTACTCCGTCTGTCTGCCTTGGGGCCGGGGTGCAGCGCTACCTCC
AGGAGGCTGCCGGGAGGCCATACACCCCCAGCCGTCCACTCCAACACGCCAGTCACC
CAGGCCGCCAGGGCAACCTGCCGTCCCTATTGCCGCCCTGGCGGGTGCCTGGC
CGCGCTGGCTGCCGTGGGGCAGCCTACTGTGTGCCGGGGGGCCATGGCAGCG
CTCAGGACAAAGGGCAGGTGGGGCAGGGCTGGGCCACTGGAACTGGAGGGAGTGAAGGTC
CCCTTGAGGCCAGGCCAGGCCAGGCCAACAGAGGGCGGTGGAGAGGCCCTGCC
GTGTGAGGTGCCACTCATGGCTTCCCAGGGCTGGCCTCAGTCACCCCTCCACGCC
CCTACATTAAGCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCTGCTGCCACACCACGTAAGTCTCAGTCCAAACCTCGGGATGTGCGAGA
CAGGGCTGTGTGACCAACAGCTGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGCAGGGCAGGCCCTGCCATGTGCTGGTAAC
GCATGCCCTGGCCCTGCTGGCTCTCCCACCTCCAGGCCAGGCCCTGGGGCAGTGAAGGAAG
CTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGACTCTAGTCTTGCC
AAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTAGGAACATGTTGCTTTTAA
AATATATATATATTATAAGAGATCCTTCCCATTATTCTGGAAAGATGTTTCAA
AGAGACAAGGACTTGGTTTGTAAGACAAACGATGATGATGAAGGCC
ATAAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLPLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN
GITMLDASSFAGLPGQLLDSLQNQIASLRLPRLLLDLSHNSLLALEPGILD TANVEALRL
AGLGLQQQLDEGLFSRRLRNLDLSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNLSQLALPGDLSGLFPRLLLAAARNPFNCVCPLSWFGP WVRESHVTLASP
EETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAP
ATEAPS PPPSTAPPTVGPVPQPQDCCPPSTCLNGGTCHLGTRHHACLCPEGFTGLYCESQM**Q**
GTRPSPTPVTPRPPRSLTGIEPVSPSLRVGLQRYLQGSSVQLRSLRTYRNLSGPDKRLV
TLRLPASLAEYT VQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE
GNLPLLIA PALAAVLLA ALAAVGAAYCVRRGRAMAAAQDKQVGPGAGPLELEGVKVPLEP
GPKATEGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACGCCGTACCCCTAACCGCCCCGCCACC
TCCTTGCTACCCCACCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
ATCTCCTTCTTGCTAGCCCCAAAGGGCCTCCAGGCAACATGGGGGCCAGTCAGAGAGC
CGGCACACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGCAGCTCTGGGGCCGTGGCTTGCC
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCCCTCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCGGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGAGAATGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCCTGCACCTGGTTCCCATTAAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTAGGCGTGGAGAGGCCTAC
AGGCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTATCTGCTGTATGCCAGGTC
CTGTTCAAGACGTGACTTCAACCATGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCAGGGCTACACAGCT
GCTATAGCGCAGGTGTCTCCATTACACCAAGGGATATTCTGAGTGTATAATTCCCCGG
GCAAGGGCGAAACTTAACCTCTCCACATGGAACCTTCTGGGTTGTGAAACTGTGAATT
GTGTTATAAAAAGTGGCTCCAGCTTGGAAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTCCTGGGTTGGCTC
CCCGTTCCCTCACTTTCCCTTTCAATTCCCACCCCTAGACTTGATTTACGGATATCTTG
CTTCTGTTCCCCATGGAGCTCCG

FIGURE 28

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27433, pI: 9.85, NX(S/T): 2
MPASSPFL LAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQLRREV
SRLQGTGGPSQN GEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVR IQDAGVYLLYSQVLFQDVTFMGQVVSREG
QGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVII PRARAKLNLSPHGTFLGFVKL
```

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

FIGURE 29

CACTTTCTCCCTCTTCTTACTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGTGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCCCACCCCTCCTCTGCAC TGCCGTCCCGGAAGACCTTTCCTGCTCTGTT
TCCTTCACCGAGTCTGTGCATGCCCGGACCTGGCCGGAGGAGGCTTGGCCGGCGGAGA
TGCTCTAGGGGGCGCGCGGGAGGAGCGGCCGGGGACGGAGGGCCCGCAGGAAGATGGGC
TCCCGTGGACAGGGACTCTGCTGGCGTACTGCCTGCTCCTTGCCTCTGGCCTGGT
CCTGAGTCGTGTGCCCATGTCCAGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAAACATGAAAATACAGGCCAGTCAG
GACCAGGGCTCCCTGCTTCCGGTGCCTGCGCTGCTGTGACCCCCGTACCTCCATGTACCC
GGCGACCGCCGTGCCCATCAACATCACTATCTGAAAGGGAGAAGGGTGACCGCGGAG
ATCGAGGCCTCCAAGGGAAATATGGCAAACAGGCTCAGCAGGGGCCAGGGCCACACTGGA
CCCAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTGGTGGGCCGGAAGAACCCATGCACAGCAACC ACTACTACCAGACGGT GATCTTCG
ACACGGAGTCGTGAACCTCTACGGACCCTCAACATGTTCACCGGAAGT TCTACTGCTAC
GTGCCCGCCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCCAGAAGGAGACCTACCT
GCACATCATGAAGAACGAGGAGGGAGGTGGT GATCTTGTTCGCGCAGGTGGCGACCGCAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGTACGCC
TACAAGGGCGAACGTGAGAACGCCATCTCAGCGAGGAGCTGGACACCTACATCACCTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCTAGCTGGCCGCCACCTCCTTCCTCGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGATCCCTGACTCCGACTC
CCTGGCTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAAGGGGGGACCCGC
GAGAACCTCTGGACCTTCCGGCCCTCTGCACACATCCTCAAGTGACCCCGCACGGC
GAGACGGGTGGCGCAGGGCGTCC CAGGGTGGCACC CGGGCTCCAGTCTTGAAATA
ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTTGTCTTCCAGCCAGCCTGCTGGCTCCAAAGAGAGAGGCCTTTCAGTTGAG
ACTCTGCTTAAGAGAACGCTCAAAGTTAAAGCTCTGGGTCAAGGGAGGGGCCGGGCGAGG
AAACTACCTCTGGCTTAATTCTTTAAGCCACGTAGGAACCTTCTTGAGGGATAGGTGGACC
CTGACATCCCTGTGGCCTTGCCTGCCCAGGGCTCTGCTGGTCTTCTGAGTCACAGCTGCGAGGT
GATGGGGCTGGGCCAGGCCTGAGCCTCCCAGGGACAGCTGAGCCCTGCCTTGGC
TCCAGGGTGGTAGAGCAGCGAAGGGCTCCTGACAGTGGCAGGGACCCCTGGTCCCCA
GGCCTGCAGATGTTCTATGAGGGCAGAGCTCCTGGTACATCCATGTGTGGCTTGCTCC
ACCCCTGTGCCACCCAGGCCCTGGGGGTGGTCTCCATGCCTGCCACCCCTGGCATCGGCT
TTCTGTGCCGCCTCCCACACAAATCAGCCCCAGAAGGCCCGGGCCTGGCTTGTGTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGCTAAGCATCACCGCTT
CCACGTGTGTTGTTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCTACTGCC
CATCCAGGCCTCTGACCACTAGCCTGAGAGGGCTTTCTAGGCTTCAGAGCAGGGAGAG
CTGGAGGGGCTAGAAAGCTCCGCTGTGTTCTCAGGCTCTGTGAGGCTCAGTC
AGACCAGAGTCAAGAGGAAGTACACGTCCAATCACCGTGTCAAGGATTCACTCTCAGGAGC
TGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
GTGTCTCCACGGTGCTCTGCCCTGCCATGCCACCCAGACTCTGATCTCCAGGAACCC
ATAGCCCCCTCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTGCTACCCGCTGGGCC
CCCAAAACCCCGCTGCCCTCTTCCCTCCCCCATCCCCCACCTGGTTTGACTAATCCTGC
TTCCCTCTCTGGGCCTGGCTGCCGGATCTGGGTCCTAAGTCCCTCTCTTAAAGAAACTT
CTGCGGGTCAAGACTCTGAAGCCGAGTTGCTGTGGCGTGCCTGGAGCAGAGGCCACACTC
GCTGCTTAAGCTCCCCAGCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTCAA

FIGURE 30

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFHGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP
```

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GC GGAGCATCCGCTGCGGTCTCGCCGAGACCCCCGGCGATTGCCGGTCTTCCCGGG
GCGCGACAGAGCTGCCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCTCGACGCCA
GAGAGAAATCTCATCATCTGTGCAGCCTCTAAAGCAAACATAAGACCAAGGGAGGATTAT
CCTTGACCTTGAAAGACCAAAACTAAACTGAAATTAAAATGTTCTCGGGGAGAAGGGAG
CTTGACTTACACTTGGTAATAATTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAATC
AGAGGCAATGAGCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTGCTGTTCAAC
AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTCGACACTCGAAAAACAGCTA
GACAACCCAACTGCTACCTATTCTGTCCTAACGAGGAAGCCTGCTCCATTGAAACCAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTCAAGCAGTCACCCCC
CCAAGAGTTACCCCAGGAAGATTCTCTTACATGGCAATTTCACAAGCAGTCACCCCC
TAGCCCCATCATCACACAGATTATCAAAGCCCACCGATATCTCATGGAGAGACACACTTCT
CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAGATGGATGAAGCAAGTGC
GCTCCTGCTTATAAGGAAAAGGCCATTCTCAGAGTTACAACATTCTCTGATCAAGAAA
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
CATACCACCTCGGCTACTCCAAAGCCCACCCCTCTACCCACCAATGCTCAGTGACACC
TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACACTGTC
AGCCTCCCACGACCCCTCATTTCTACAGTTTACACGGGCTGCGGCTACACTCCAAGCAATG
GCTACAACAGCAGTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
AACCATAACGTTACAGAAATCTCAAACCTTAACCTTGAAACACAGGAAATGTGTATAACCC
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTGGGAAGGT
AGGGAGGCCAGTCCAGGCAGTTCTCCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCC
ATTGAAAAATGGCTTCTTATCGGGTCCCTGCTTTGGTGTCTGTTCTGGTGTAGGCC
TCGTCCCTGGGTAGAATCCTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
TATTGATCAATGGATCTATGTGGACATCTAGGATGGAACCTGGTGTCTCTTAATTCTT
TAGTAACCAGAACCCAAATGCAATGAGTTCTGCTGACTGCTAGTCTTAGCAGGAGGTTG
TATTGAAAGACAGGAAAATGCCCTCTGCTTCTGCTTTCTTTTTGGAGACAGAGTCTT
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGAACCTCCGTCTC
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCTAAAGTATCTGGGATTACAGGCATGTGCC
CCACACCTGGGTGATTTGTATTTAGTAGAGACGGGTTTACCATGTTGGTCAAGGCTG
GTCTCAAACCTGACCTAGTGATCCACCCCTCTGGCCTCCAAAGTGCTGGATTACAGG
CATGAGGCCACCACAGCTGGCCCCCTCTGTTTATGTTGGTTTGAGAAGGAATGAAGTG
GGAACCAAATTAGGTAAATTGGTAATCTGTCTAAATATTAGCTAAAACAAAGCTCT
ATGTAAGTAATAAGTATAATTGCCATATAAAATTCAAACCTGGCTTTATGCAA
GAAACAGGTTAGGACATCTAGGTCCAATTCACATTCTGGTCCAGATAAAATCAAC
TGTTTATATCAATTCTAATGGATTGCTTTCTTTATATGGATTCCCTTAAAACATTATT
CCAGATGTAGTTCCATTAAATATTGAATAATCTTTGTTACTCAA

FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTLRLSASQNCLKSLEDVVIDIQSSL SKGIRGNEPVYTSTQED
CINS CCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTA SWE GREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSR LDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGCTGGTATTGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATGGGGAGAGGCCTGTCCCAAAGCTCCAGTCC
CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCCTACAGGTTA
CTCAGCGGAGGTGGCAGAACAGCAAGTACGCCAAAATCTGCTTGAGGATAACCTACTTATGGG
AGAACAGCTGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACGGAA
ATGTGACAGCAACACGATGTTGATATGTATGAAGGCATAACTCTGGACCGATGACAAG
TTTATTCAAGAGTGCTGCTCCAAAATCCCTGCTTCATGGTACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAACGACTTGGAAAGTAAAGAAATCAGGAACA
TGAAATTCAAGGTCTAGCTGGTATTATTGCAGCAAAAGGCTTGGAACTCCCTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGTGACACTGCAGGGCCTGAGTAAAT
GTGTTCTGTATAACAAATGCAGCTGGAATCGCTCAAGAACATCTTATTTCTAAATCCAACA
GCCCATATTGATGAGTATTGGGTTGTTGTAACCAATGAACATTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTATACCAAGTATTTATGTAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTCPSPDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMDYEGDNNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125